

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 10:08:33 ; Search time 2532 Seconds

(without alignments)
17692.226 Million cell updates/sec

Sequence: 1 atgagcgttgtaagttgca.....gtacatcaagggtctctaa 2766

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Labeling - first 45 summaries

1: em_estba:*
2: em_estbm:*
3: em_estbn:*
4: em_estbu:*
5: em_estbv:*
6: em_estbp:*
7: em_estbr:*
8: em_estbs:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_estl3:*
12: gb_estl4:*
13: gb_estl5:*
14: gb_estl6:*
15: em_estfun:*
16: em_estfm:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_luv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813.8	29.4	887	13	BI913344 603178823
2	743.4	26.9	791	13	BI523145 603175911
3	739.8	26.7	792	13	BI522813 603175911
4	673.2	24.3	775	14	BQ770745 UI-M-F10-
5	657	23.8	665	14	BQ189572 UI-E-EJ1-
6	560.2	20.3	676	10	BB280958 BB280958

C	7	553.6	20.0	1062	17	CNS04DXR	AL286344 Tetradon
	8	516	18.7	527	12	BG910325	BG910325 602805921
	9	416.4	15.1	718	13	BI756778	BI756778 603024449
	10	407.8	14.7	475	12	BR190598	BR190598 237175 MA
	11	407.4	14.7	499	17	BH349372	BH349372 CH230-32M
	12	372.8	13.5	3063	11	BC023215	BC023215 Homo sapi
	13	368.2	13.3	817	13	BI551720	BI551720 603197384
	14	361.8	13.1	655	12	BG819145	BG819145 602781252
	15	359.4	13.0	677	12	BG293782	BG293782 602390677
	16	359	13.0	569	13	BI906774	BI906774 603064517
	17	345	12.5	638	12	BG772726	BG772726 602720880
	18	338.2	12.2	1020	17	CNS03928	AL265769 Tetradon
	19	320	11.6	384	17	AZ258968	AZ258968 RPCI-23-1
	20	319.8	11.6	550	9	AA511690	AA511690 v916a04.r
	21	303	11.0	462	9	AL712986	AL712986 DXF2p686T
	22	295.8	10.7	693	10	BB648018	BB648018 BB648018
	23	294.2	10.6	551	17	FR0052027	AL688306 Fugu rubr
	24	291.4	10.5	876	9	AL666430	AL666430 Fugu rubr
	25	270.4	9.8	590	14	BQ187487	BQ187487 UI-E-EJ1-
	26	267.2	9.7	1098	17	CNS04YRK	AL309449 Tetradon
	27	261	9.4	261	14	BM930281	BM930281 UI-E-EJ1-
	28	258.8	9.4	1010	13	BM547961	BM547961 AGENCOURT
	29	257.8	9.3	421	12	BG554724	BG554724 dac30d12.
	30	253.8	9.2	486	12	BF515586	BF515586 UI-H-BW1-
	31	240.6	8.7	1052	17	CNS01EN3	AL174504 Tetradon
	32	237.8	8.6	514	12	BG371210	BG371210 Tetradon
	33	237.6	8.6	753	13	BI875890	BI875890 f164d02.y
	34	233.6	8.5	668	14	BQ284787	BQ284787 f294e06.x
	35	213.6	7.7	885	17	CNS013JA	AL102928 Drosophila
	36	208.4	7.5	689	14	BQ263135	BQ263135 f294e06.y
	37	208.4	7.5	731	13	BI144538	BI144538 BJA44538
	38	206.2	7.5	455	10	AV952826	AV952826 AV952826
	39	201.8	7.3	1090	17	CNS05E11	AL333770 Tetradon
	40	200.8	7.3	863	17	CNS030NR	AL253584 Tetradon
	41	198.2	7.2	481	14	BQ339473	BQ339473 PM1-NN022
	42	198.2	7.2	481	14	BQ339495	BQ339495 PM1-NN022
	43	193.8	7.0	493	10	AW346838	AW346838 29591 MAR
	44	189.2	6.8	544	9	AA733833	AA733833 v004f02.r
	45	187.8	6.8	750	17	CNS04MA3	AL297156 Tetradon

ALIGNMENTS

RESULT 1
BI913344 887 bp mRNA linear EST 16-OCT-2001
LOCUS 603178823F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243308 5',
DEFINITION mRNA sequence.
ACCESSION BI913344
VERSION BI913344.1 GI:16177710
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 887)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1613 row: m column: 05
High quality sequence stop: 782.
Location/Qualifiers
1. 887

FEATURES
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5243308"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; site_1: NotI;
site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

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BASE COUNT 236 a 204 c 252 g 195 t

Query Match 29.4%; Score 813.8; DB 13; Length 887;

Best Local Similarity 97.2%; Pred. No. 2.5e-205;

Matches 860; Conservative 0; Mismatches 22; Indels 3; Gaps 3;

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Y 916 GGAAGAAGAGTGTGATCCCGCAGAGATGATCCGGATTCTCAAGATCTGAAGCA 975
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Db 1 GGAAGAAGTGTGATCCCGCAGAGATGATCCGGATTCTCAAGATCTGAAGCA 60
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QY 976 AAACACCAGAGAGACTTATGATCAGCTGGTGGATGGCCAAATTAATGCTCTTCC 1035
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Db 61 AAACACCAGAGAGACTTATGATCAGCTGGTGGATGGCCAAATTAATGCTCTTCC 120
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QY 1036 CACCAACAGAGAGCGCGCTTCTACCGTATCCAGGCACTCGTATGATGACTGTGCA 1095
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Db 121 CACCAACAGAGAGCGCGCTTCTACCGTATCCAGGCACTCGTATGATGACTGTGCA 180
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QY 1096 GGCATATCCGAGAAACATGAGCAGCAACAAGCCAAAGCGCTCCAGATAGCCAG 1155
|||||
Db 181 GGCATATCCGAGAAACATGAGCAGCAACAAGCCAAAGCGCTCCAGATAGCCAG 240
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QY 1156 GTGCACACGATGAGCCCTGAGGACTTATTTCCAAAGCTCTTGTGACCACTGTTCTAC 1215
|||||
Db 241 GTGCACACGATGAGCCCTGAGGACTTATTTCCAAAGCTCTTGTGACCACTGTTCTAC 300
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QY 1216 CAGTGCCTGAGAACTGTGGGCTGTACTCTCTGACAGTGTGAGAAAGGGGAGACATG 1275
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Db 301 CAGTGCCTGAGAACTGTGGGCTGTACTCTCTGACAGTGTGAGAAAGGGGAGACATG 360
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QY 1276 TCAAAGACCATGTATGTGACTACAAAACAGAGATGTTCTGCCAATGACGGGCTGAC 1335
|||||
Db 361 TCAAAGACCATGTATGTGACTACAAAACAGAGATGTTCTGCCAATGACGGGCTGAC 420
|||||
Y 1336 TATGAGTTCACAGAGGCGCGGTGTTCTGAAGCCAGAGAGACCACAGAGATGTTCTCC 1395
|||||
Db 421 TATGAGTTCACAGAGGCGCGGTGTTCTGAAGCCAGAGAGACCACAGAGATGTTCTCC 480
|||||
QY 1396 GTGGGCATTAATGATGACGACATTTTGTGAGAGATGAACACTTCTTGTAAAGTTGAGC 1455
|||||
Db 481 GTGGGCATTAATGATGACGACATTTTGTGAGAGATGAACACTTCTTGTAAAGTTGAGC 540
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QY 1456 AATGCGGCATAGAGAGGAGACAGCCAGAGAGGAGATGCTCCAGCAATTTCAACAGT 1515
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Db 661 GATGACCATGAGGAGCATCTTTCATTTGAATGTGATACATATTCATGAGAGATTT 719
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QY 1636 GGTGTATAGAGATCAAGGTTCTGCGGACATCAGAGTGGCGGGGTACAGTATGTCCTCC 1695
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Db 720 GGTGTATAGAGATCAAGGTTCTGCGGACATCAGTGTGCCGGGGTACAGTATGTCCTCC 779
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QY 1696 TTT-AGCAGACTAGAGAGGACAGCCAGCGTGGTGAGGACTTTGAGACACATATAG 1754
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Db 780 TTTGAGAGACAGAGAGGAGACAGCCAGCGTGGTGAGGACTTTGAGACACATATAG 839
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QY 1755 GGAGTGGAAATTCAGAAATGATGAANAACCTGTAAGAGGT 1799
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Db 840 GGAGTGGAAATTC-CGACTGGTGAACCTGTGAACCATTCACAGGT 883
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RESULT 2

BI523145/c 791 bp mRNA linear EST 29-AUG-2001

LOCUS 60317591R1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240066 3',

DEFINITION mRNA sequence.

ACCESSION BI523145

VERSION BI523145.1 GI:15347937

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 791)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: LNA11605 row: f column: 03

High quality sequence stop: 790.

Location/Qualifiers

FEATURES

source

1..791

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5240066"

/clone_lib="NIH_MGC_121"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-Sport6; site_1: NotI;

site_2: EcoRV (destroyed); RNA source anonymous pool of 3

fetal brains, female age 20 weeks, female age 24 weeks,

and male age 26 weeks. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

0.7-3.5 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 017. Note:

this is a NIH_MGC Library."

BASE COUNT 186 a 217 c 220 g 166 t 2 others

ORIGIN

Query Match 26.9%; Score 743.4; DB 13; Length 791;

Best Local Similarity 98.5%; Pred. No. 1.4e-186;

Matches 782; Conservative 0; Mismatches 7; Indels 5; Gaps 3;

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QY 1839 TTTCTTATGCTCCCTTGTGTAACCGAATGATGAAC-GTGAATATCAGATGTGACG 1897
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Db 791 TTTCTTATGCTCCCTTGTGTAACCGAATGATGAACNGTGAATATCAGATGTGACG 732
|||||
QY 1898 ACAGAACTGATGATGAGAGAGAGCCAGAGAGATGACAGATGGGAAAGCCAG 1957
|||||
Db 731 ACAGAACTGATGATGAGAGAGAGAGCCAGAGAGATGACAGATGGGAAAGCCAG 672
|||||
QY 1958 TATTGGTGAACACCCCAACTAGAGCATCTTGAAGAGTCTATGAGTTCAAGACTA 2017
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Db 671 TATTGGTGAACACCCCAACTAGAGCATCTTGAAGAGTCTATGAGTTCAAGACTA 612
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Oy 2018 CGGTGGACAACTGATCAAGAGAACAAACCTGGCTTGGTGTGGGACCAATCTCTGGA 2077
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Oy 2078 GGGACCAAGTTCATGAGAGCCATCACCCTGATGTCAGCAGGGGATGAGATGAGATGAAT 2137
    |||
Db 551 GGGACCAAGTTCATGAGAGCCATCACCCTGATGTCAGT---GACGGGATGAGATGAGATGAAT 495
Oy 2138 CGGGGAGAGAGAGCGCCCTCTGCTTGTGACATGACATGACATCTCCAGATGCTCTCT 2197
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Db 494 CGGGGAGAGAGAGCGCCCTCTGCTTGTGACATGACATGACATCTCCAGATGCTCTCT 435
Oy 2198 GGAAGGTGCTGTTTGGCTGTGTCGCCCAACAGAGTACTGCAAGGCTGGGCTGCTTGC 2257
    |||
Db 434 GGAAGGTGCTGTTTGGCTGTGTCGCCCAACAGAGTACTGCAAGGCTGGGCTGCTTGC 375
Oy 2258 CCGTCTCCATCTCATCATATGAGCATGACCGCCATCATTTGGGAGCTGGGCTGCTGCACT 2317
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Db 374 CCGTCTCCATCTCATCATATGAGCATGACCGCCATCATTTGGGAGCTGGGCTGCTGCACT 315
Oy 2318 TGGGGGACCAATGCTCAAGAGATTCAGTCAACAGCTGTTGTTTCTGGGATTTGGCA 2377
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Db 314 TGGGGGACCAATGCTCAAGAGATTCAGTCAACAGCTGTTGTTTCTGGGATTTGGCA 255
Oy 2378 CCTCTGTCCAGATAGCTTGGCCAGCAAGCTGCTCCCTCCAGATGATATGACAGAG 2437
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Db 254 CCTCTGTCCAGATAGCTTGGCCAGCAAGCTGCTCCCTCCAGATGATATGACAGAG 195
Oy 2438 CCTCATTTGGCAAGCTGAGCGGAGCAAGCGGTCATGTCCTTCTGGGATTCGGGCTG 2497
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Db 194 CCTCATTTGGCAAGCTGAGCGGAGCAAGCGGTCATGTCCTTCTGGGATTCGGGCTG 135
Oy 2498 CTTGGGCTGGGCGGCGCATCTACTGGGCTCTGAGGGAAGAGATTCAGCTGCGCG 2557
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Oy 2558 GCACACTGGCTTCTCCGTCACCCCTTTCACATCT-TTGCATTTTCTGACATCAGCTG 2616
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Db 74 GCACACTGGCTTCTCCGTCACCCCTTTCACATCTCTGACATCTCTGACATCAGCTG 15
Oy 2617 CTTCTGTACCGAAG 2630
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Db 14 CTTCTGTACCGAAG 1

RESULT 3
B1522813 792 bp mRNA linear EST 29-AUG-2001
LOCUS 603175911F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240066 5',
DEFINITION B1522813 792 bp mRNA linear EST 29-AUG-2001
ACCESSION B1522813 Homo sapiens cDNA clone IMAGE:5240066 5',
VERSION B1522813.1 GI:15347605
KEYWORDS mRNA sequence.
SOURCE EST.
ORGANISM human.
            Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
            1 (bases 1 to 792)
            NIH-MGC http://mhc.ncl.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1605 row: f column: 03
            High quality sequence stop: 778.
            Location/Qualifiers
FEATURES
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/clone="IMAGE:5240066"
/clone_11b="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; Site:1: NotI;
Site:2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is 0.190-0.7 kb,
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH-MGC Library."
BASE COUNT      202 a      179 c      227 g      184 t
ORIGIN
Query Match      26.7%; Score 739.8; DB 13; Length 792:
Best Local Similarity 98.7%; Pred. No. 1.2e-185;
Matches 767; Conservative 0; Mismatches 7; Indels 3; Gaps 2:
Oy 993 CTTAGATCAGCTGGTGGAGTGGCAATTAATCTATGCTCTTCCACCAAGAGAGCCG 1052
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Db 1 CTTAGATCAGCTGGTGGAGTGGCAATTAATCTATGCTCTTCCACCAAGAGAGCCG 60
Oy 1053 CGCCTTTCACCGTATCCAAAGCCACTGATGATGACTGTGTCAGGCAATATCTGAAAG 1112
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Db 61 CGCCTTTCACCGTATCCAAAGCCACTGATGATGACTGTGTCAGGCAATATCTGAAAG 120
Oy 1113 ACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1172
    |||
Db 121 ACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Oy 1173 TGAGGACTTATTTCCAAAGTCTTCTTGTGACCATTTCTTACAGTGGCTGAGAACTG 1232
    |||
Db 181 TGAGGACTTATTTCCAAAGTCTTCTTGTGACCATTTCTTACAGTGGCTGAGAACTG 240
Oy 1233 TGGGGCTGTACTCTGACAGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1292
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Db 241 TGGGGCTGTACTCTGACAGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Oy 1293 GGACTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1352
    |||
Db 301 GGACTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Oy 1353 CACGGTGTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1412
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Db 361 CACGGTGTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Oy 1413 CGACATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1472
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Db 421 CGACATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Oy 1473 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1532
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Db 481 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Oy 1533 TGTGCTAGGCTCCCTTGTGTGTCACAGTATACATCTTGGAGATGAGACATCAGAGAT 1592
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Db 541 TGTGCTAGGCTCCCTTGTGTGTCACAGTATACATCTTGGAGATGAGACATCAGAGAT 600
Oy 1593 CTTCACTTTTGAATGATGATATGATGATGATGATGATGATGATGATGATGATGATG 1652
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Db 601 CTTCACTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Oy 1653 GATTTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1711
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Db 661 GATTTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Oy 1712 GGACAGCCAAAGGCTGGCGGT--GAGGACTTTGAAGACATATAGGGAGTTGGAATT 1766
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DB	721	GGACGACCAAGGCTGGCGTGCAGCGACTCTGTAACACATATTTGGGAGTTGGAAAT	777
RESULT 4	B0770745	775 bp	RNA linear EST 26-JUL-2002
LOCUS	B0770745		
DEFINITION	UI-M-F10-BYV-c-07-0-UI.r1 NIH_BMAP_F10	Mus musculus	CDNA clone
IMAGE	6400062 5'		mRNA sequence.
ACCESSION	B0770745	GI:21979219	
VERSION	B0770745.1		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 775)		
TITLE	NIH-MGC http://mgc.ncl.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs-remail.nih.gov		
	Tissue Procurement: Dr. Jim Lin, University of Iowa		
	CDNA Library preparation: Dr. M. Bento Soares, University of Iowa		
	CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa		
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa		
	Clone Distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	This clone was contributed by the Brain Molecular Anatomy Project		
	(BMAP)		
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SOURCE	Location/Qualifiers		
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	/dev_stage="embryo 12.5dpc"		
	/lab_host="DH10B (T1 phage resistant)"		
	/note="Organ: Brain; Vector: PYX-Asc; Site:1: EcoR I; Site:2: Not I; The library was constructed according		
	Bonaldi, Lennon and Soares, Genome Research, 6:791-806,		
	1996. Denatured RNA was size fractionated on a 1% agarose		
	gel. First strand cDNA synthesis was primed with oligo-dT		
	primer containing a Not I site. Double strand cDNA was		
	size selected according to mRNA size fraction. Ligated		
	with EcoR I adaptor, digested with NotI and then cloned		
	directionally into PYX-Asc vector. The library tag		
	sequence located between the Not I site and the polyA tail		
	is CAGCAGCAGC. This library was created for the University		
	Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the		
	Developing Mouse Nervous System', supported by National		
	Institute of Mental Health (NIMH), Hemlin Chlin, Ph.D.,		
	program coordinator."		
BASE COUNT	168 a 185 c 202 g 219 t	1	others
ORIGIN			
Query Match	24.3%	Score 673.2	DB 14: Length 775;
Best Local Similarity	91.7%	Pred. No. 6.8e-168;	
Matches 711:	Conservative 0;	Mismatches 64;	Indels 0; Gaps 0;
OY	66 GCTCTTCTGATGAGTCTCTTCGAGCAGAGGCTGGTCTCAGGAGCGTGCACAGCAGG	125	
Db	1 GCTCTTCTGATGATGCTCTTCGAGCAGAGGCTGGTCTCAGGAGCGTGCACAGCAGG	60	
OY	126 GCAGACATGATGCTCTTCAGGGTCTATCGGACTGCAGAGAGGGTGTCTATTCGCAT	185	
Db	61 GCAGACATGATGCTCTTCAGGGTCTATCGGACTGCAGAGAGGGTGTCTATTCGCAT	120	
OY	186 CTGCTACCCGGAGACCTTCCCTTGGGGACAAAGTTCCAGGGTCTATTTTGT	245	

Db	121	CTGGATATCCAGAAACCCCTTCCCTTGGGGAGACAAGATTGGCAGGGTCATTTGCTATTTTGT	180
OY	246	GGCCCTGATATACATATGTTCTTGGGGTGTCCATCATCTTGGTGACCGCTTCATGGCATAT	305
Db	181	GGCCCTGATATACATATGTTCTTGGGGTGTCTATATTTGCTGCATTCATTCATGGCATTTAT	240
OY	306	TGAATCTATACCTTCCAAAGAGAGGAGGTGACATTTAAGAAACCCATNGGAACAG	365
Db	241	TGAATCTATATCTTCCCAAGAGAGGAGAGGTGACCATCAAGAAAGCCCAATGGAGAACAG	300
OY	366	CACACACCATATATCGGGTCTGGAAATGAACACTGTCTCCAAACCTTGATAGGCCCTGGG	425
Db	301	CACACATCAATATGGGGATGATGAATGAACACTGTCTCCAAATCTGACCCATGATGGCCCTGGG	360
OY	426	TTCTCTGCTGCTCTGAGATATCTCTCTTTAAATTGAGGTGTGTGTCATGGGTTCATTGC	485
Db	361	CTCTTCTGCTCCAGAGATTCTCTCTCTTTAATTGAGGTGTGTGTCACGGGTTCATTGC	420
OY	486	TGTGTATCTGGGACCTTTTACCATTTGTAGGAGTGTGACACCTTCAACATGTTTCATCATAT	545
Db	421	TGTGTATCTGGGACCATCTTACCATGTTGGGCGTGTACCCCTTCAACATGTTTCATCATAT	480
OY	546	TGGCATCTGTGTCTTACGTGATCCAGACGAGAGACTGCGAAGATCAAGCATCTACGAGT	605
Db	481	TGGCATCTGTGTCTTATGTGATCCAGATGGGAGACTGGAAGATCAAGCATCTACGAGT	540
OY	606	CTTCTTCATCACCGCTGTTGGAGTATCTTTGCCATATCTGGCTCTATATGATTTCTGGC	665
Db	541	CTTCTTCATCACCGCTGTTGGAGTATCTTTGCCATATCTGGCTCTATATGATTTCTGGC	600
OY	666	AGTCTTTCCTCCCTGGTGTGTGCTCAGGTTTGGGAAGCCCTCCACTGCTCTCTCTTCTTCC	725
Db	601	AGTCTTTCCTCCCTGGTGTGTGCTCAGGTTTGGGAAGCCCTCCACTGCTCTCTCTTCTTCC	660
OY	726	AGTGTGTCTCTCTTGGGCTGGCTGGCAGATTAACGACTGCTCTTCTCAATATCATGCA	785
Db	661	CGTGTGTCTCTCTGGGCTGGGCTGGTGTGATGATTAAGGACTGCTCTTCTCAATATCATGCA	720
OY	786	CAAAAAGTACCGCAGACAAACACCGAGGAATTATCATAGAGACAGAGGCTGAC	840
Db	721	CAGAAAATACCGCAGACAGATTAACACCGAGGAATTATCATAGAGACAGAGGCTGAC	775
RESULT 5			
LOCUS	B0189572	665 bp	linear
DEFINITION	UI-E-EJ1-aka-f-22-0-UI-r1 UI-E-EJ1 Homo sapiens cDNA clone		EST 30-APR-2002
ACCESSION	B0189572		
VERSION	B0189572.1	GI:20365123	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 665)		
	Bonaldi,M.F., Lennon,G. and Soares,M.B.		
	Normalization and subtraction: two approaches to facilitate gene		
	discovery		
	Genome Res. 6 (9), 791-806 (1996)		
JOURNAL	97044477		
MEDLINE	Contact: Soares, MB		
COMMENT	Program for Rat Gene Discovery and Mapping		
	University of Iowa		
	451 Eckstein Medical Research Building Iowa City, IA 52242, USA		
	Tel: 319 335 8250		
	Fax: 319 335 9565		
	Email: msources@blue.weeg.uiowa.edu		
	Tissue Procurement: Dr. Gregg Hageman		
	cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa		
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa		
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa		
	Clone Distribution: Researchers may obtain clones from Research		

Genetics (www.resgen.com).
Seq primer: M13 REVERSE.

FEATURES
Source

Location/Qualifiers
1. 665
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-E11-aka-f-22-0-UI"
/clone_lib="UI-E-E11"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life technologies) (TI phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; UI-E-E11 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)₁₈ tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAACTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
BASE COUNT 127 a 198 c 179 g 161 t
ORIGIN

Query Match 23.8%; Score 657; DB 14; Length 665;
Best Local Similarity 99.2%; Pred. No. 1.3e-16;
Matches 660; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1964 GTGAACACCCCAACTAGAGATCATATGAGAGAGCCATGATGATCAAGACTACGAGG 2023
DB 1 GTGAACACCCCAACTAGAGATCATATGAGAGAGCCATGATGATCAAGACTACGAGG 60
OY 2024 ACAACATGATCAAGAAGACAACACTGCGCTGTGTGGGAGCCATTCTCTGGAGGACC 2083
DB 61 ACAACATGATCAAGAAGACAACACTGCGCTGTGTGGGAGCCATTCTCTGGAGGACC 120
OY 2084 AGTTATGAGGCCATACCGTCACTGACGACGAGGAGATGAGATGATGATCCGGGG 2143
DB 121 AGTTATGAGGCCATACCGTCACTGACGACGAGGAGATGAGATGATGATCCGGGG 180
OY 2144 AGGAGAGGCGCCGCTGCTTGAAGTACGATGATGATGATGATGATGATGATGATGATG 2203
DB 181 AGGAGAGGCGCCGCTGCTTGAAGTACGATGATGATGATGATGATGATGATGATGATG 240
OY 2204 TGCTGTGCTGCTGTGCGCCACAGAGTACTGCGACGGTGGGCTGCTTGCCTGT 2263
DB 241 TGCTGTGCTGCTGTGCGCCACAGAGTACTGCGACGGTGGGCTGCTTGCCTGT 300
OY 2264 CCATCTCTATCTTTGGGATGCTACCGCCATATTGGGAGCTGGCTGCACTTGGCT 2323
DB 301 CCATCTCTATCTTTGGGATGCTACCGCCATATTGGGAGCTGGCTGCACTTGGCT 360
OY 2324 GCACCATGGTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2383
DB 361 GCACCATGGTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
OY 2384 TCCGAGATACGTTTGCACCAAGAGTGTGCTCCAGAGATATATGACAGAGCTCCCA 2443
DB 421 TCCGAGATACGTTTGCACCAAGAGTGTGCTCCAGAGATATATGACAGAGCTCCCA 480
OY 2444 TTGGCAACCTGACGGGACCAAGCCGCTCAATGCTTCTGGGACATGGCTGGCTGGT 2503
DB 481 TTGGCAACCTGACGGGACCAAGCCGCTCAATGCTTCTGGGACATGGCTGGCTGGT 540

OY 2504 CCGTGGCCGCGATCTACTGAGGCTGACAGGACAGAGATTCACAGTGTGGCCGACAC 2563
DB 541 CCGTGGCCGCGATCTACTGAGGCTGACAGGACAGAGATTCACAGTGTGGCCGACAC 600
OY 2564 TGGCTTCTCCGCTCAACCCCTTACACATCTTGCATTTTGTCTGCATCAGCGTCTTGT 2623
DB 601 TGGCTTCTCCGCTCAACCCCTTACACATCTTGCATTTTGTCTGCATCAGCGTCTTGT 660
OY 2624 ACCGA 2628
DB 661 TACGA 665

RESULT 6
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BB280958 676 bp mRNA linear EST 31-AUG-2001
BB280958 RIKEN full-length enriched, adult retina Mus musculus cDNA
clone A930029A02.3 similar to U53420 Rattus norvegicus
sodium-calcium exchanger form 3 (NCX3) mRNA, mRNA sequence.
BB280958.2 GI:15411103
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 676)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyu,T.,
Muramatsu,M., and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jul 9, 2000 this sequence version replaced gi:8981407.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wag1,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Y., and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka,I., Kiyosawa,H., Konno,S., Saito,T., Shinagawa,A., Aizawa
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,
Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, 172-L86 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.

OY	327	GAGGAGGTGGCAATTAAGAACCACAAATGSGAAMCCAGACAACACTATTTCGGGCTCG	386
Db	882	GCGGGAATCATCATCAAAGGCCAACGAGAAACCCACACACACACATAAGGGTTTG	823
OY	387	GAATGAACCTGCTCCAACCTGACCTTATGGCCCTCGGGTTCCTCGCTCGAATACT	446
Db	822	GAAGAAACGGCTCCCAACCTCACCTTAGCCTTGGGCTGTCCGGCCCGGATGCTCT	763
OY	447	CCTCTCTTAATTGAAGTGTGTGTCATATGGGTTCATTCTGTGTATCTTGGACCTTAC	506
Db	762	GCTCTCCCTCATCGAGGCTCGGGCCAGACTTCAAGCCCAGCGAGCTGGGACCCGCAC	703
OY	507	CATTGTAGGAGTGAAGCTTCAACATGTTCATCTTCAATTTGGCATCTGATAGTGTAT	566
Db	702	CATGCTGGGCGAGCGCGGCTTCAACATGTTTGTCTATCTAGGCTGTGCTGTCCGTAT	643
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Db	583	GAGCATCTTTTCCCTACATTTGGCTCTATCATGATCTTGGCGCTGTTCACGCCCCAGGTGT	524
OY	687	CCAGTTTTGGGAAGGCGCTCTCACTCTTCTTCTTTCAGAGTGTGTCTCTGAGCGT	746
Db	523	CCAGGTGTGGGAGGGCCM-CTACGCTTGGCTTCTTCCCGCTGTGCTCTCTTGGCTTG	465
OY	747	GGTGGCAGATAAACGACTGCTCTCTTCTTACAAATATCATGACAAAAGTACCCGACAGACA	806
Db	464	GGTAGCCGAGCCGCGCGCTGTCTTCTTACAAAGTTCATGACAAAGATACCCGAACCGACAA	405
OY	807	AACCCGAGGAATTCATAGAGACAGAGGATGACACCCTAAGGGCATTTGATGATGATGG	866
Db	404	GCACCGGGGCGTATCATCGAGACGAGAGCGGAGCGCTCGAAGGGGATTCAGATGAGCGG	345
OY	867	GAATATGATGAATTCCTCATTTTCTTGTAGATGGGAAC-----CTGGTGCCTCT	911
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OY	912	GGAAGGGAAGGATGTGATGAGTCCCGCAGAGATGATCCGATTTCTCAAGATCTGAA	971
Db	284	GGAGGCGAAAGGCTGACRAGTCCCGCCGCAACATGATCCGCATCTTAAAGATCTGAA	225
OY	972	GCAAAAAACCCAGAGGAAGGACTTGATCAGTGGTGTGAGATGGGCATTTATAGTCT	1031
Db	224	GCAGAGCAACCCGGAGGAAGAGATGACACGCTGTGTGATGATGAGSAACTACACAGCCTT	165
OY	1032	TTC--CCACCAACAGAAAGAGCGCGCTTCTTA--CCGTATCCAAGCACTCTGATATGAC	1088
Db	164	CTCGTCACACAGAGAAGAGCGCGCTTCTTATCTCGCATTCGAAGCCACGCGCATATGAC	105
OY	1089	TGTGTACGCAATATCTTGAGAAACATGACAGACAGAACCCAAAGGCTCTCAGCAT	1148
Db	104	GGGGGCGGGCAACAAATGAAAAAACACAGGTGGCGGAGAGGCCAAGAGAGGCGCAGCGT	45
OY	1149	GAGCGAGGTGCACACCGATGAGCCGAGGACT	1180
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RESULT 8	BG910325	527 bp	mRNA linear EST 05-JUN-2001
LOCUS	60280592JF1	NCL_CGAP_Brn67	Homo sapiens cdNA clone IMAGE:4938316
DEFINITION	5', mRNA sequence.		
ACCESSION	BG910325		
VERSION	BG910325.1	GI:14290801	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Mammalia: Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
1 (bases 1 to 527)	NH-MGC	http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: David N. Louis, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LHAM10873 Row: 1 Column: 05 High quality sequence stop: 527.
FEATURES	source	location/Qualifiers		
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		/db_xref="taxon:9606"		
		/clone_image="4938316"		
		/clone_id="NCI_CGAP_Brn67"		
		/tissue_type="anaplastic oligodendroglioma with 1p/19q loss"		
		/lab_host="DH10B (T1 phage-resistant)"		
		/note="Organ: brain; Vector: pCMV-Sport6; Site_1: Not; Site_2: Salt; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies . Note: this is a NCI_CGAP library."		
BASE COUNT	86 a	165 c	143 g	133 t
ORIGIN				
Query Match	18.7%;	Score 516;	DB 12;	Length 527:
Best Local Similarity	99.8%;	Pred. No. 4.2e-126;		
Matches 527;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
OY	2101	ACCGCAGTGCGCAGGAGGGATAGCATGAGTGAATCCGGGAGAGAGGTGCCCTTC	2160	
Db	1	ACCGCAGTGCGCAGGAGGGATAGCATGAGTGAATCCGGGAGAGAGGTG-CCTCC	59	
OY	2161	TGCTTTGACTACGTATGCATCTCTGCACTGCTTCTGGAAGTGCTGTTGCTGTG	2220	
Db	60	TGCTTTGACTACGTATGCATCTCTGCACTGCTTCTGGAAGTGCTGTTGCTGTG	119	
OY	2221	CCCCCAGAGTAGTGCAGCGCTGGGGCTGCTTCGCCGTCCTCCATCCTCATTTGGC	2280	
Db	120	CCCCCAGAGTAGTGCAGCGCTGGGGCTGCTTCGCCGTCCTCCATCCTCATTTGGC	179	
OY	2281	ATGCTACCGCCATATTGGGGACCTGGCCTTCGCACTTGGCTGCACCATTGGTCAAA	2340	
Db	180	ATGCTACCGCCATATTGGGGACCTGGCCTTCGCACTTGGCTGCACCATTGGTCAAA	239	
OY	2341	GATTACGTCACGCGTGTGTTTCTGGCATTTGGACACTGTCGCCAGATACGTTGGC	2400	
Db	240	GATTACGTCACGCGTGTGTTTCTGGCATTTGGACACTGTCGCCAGATACGTTGGC	299	
OY	2401	AGCAAAGCTGCGCCTCCAGAGTATATGACAGACGCTTCATTGGCACAAGCTGACGGC	2460	
Db	300	AGCAAAGCTGCGCCTCCAGAGTATATGACAGACGCTTCATTGGCACAAGCTGACGGC	359	
OY	2461	AGCAAGCGCGTCAATGTCTTCTGGGCAATCGGCTGGCGCTGGTCGTCGGCCGCACTAC	2520	
Db	360	AGCAAGCGCGTCAATGTCTTCTGGGCAATCGGCTGGCGCTGGTCGTCGGCCGCACTAC	419	
OY	2521	TGGGCTTGCAGAGGACAGAGTTCACACGTGTGGCGCGGACACATGGCCTTTCGGTACAC	2580	
Db	420	TGGGCTTGCAGAGGACAGAGTTCACACGTGTGGCGCGGACACATGGCCTTTCGGTACAC	479	
OY	2581	CCTTCACACATCTTTGCAATTTGCTGCATACACGTCGCTTTTACCGA	2628	
Db	480	CCTTCACACATCTTTGCAATTTGCTGCATACACGTCGCTTTTACCGA	527	

RESULT 9
B1756778 718 bp mRNA linear EST 25-SEP-2001
LOCUS B1756778
DEFINITION 603024449F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194668 5',
mRNA sequence.
ACCESSION B1756778
VERSION B1756778.1 GI:15748356
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 718)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L14M11487 row: b column: 13
High quality sequence stop: 644.
Location/Qualifiers
1. 718
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_11d="NIH_MGC_114"
/lab_host="DH103"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
BASE COUNT 187 a 162 c 219 g 150 t
ORIGIN
Query Match 15.1%; Score 416.4; DB 13; Length 718;
Best Local Similarity 94.8%; Pred. No. 1.8e-99;
Matches 474; Conservative 0; Mismatches 21; Indels 5; Gaps 4;
Y 1887 AGATGTGACAGACAGAACTGACTATGAGAGAGAGAGAGAGAGATAGCAGAGAT 1946
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Db 215 AGATGTGACAGACAGAACTGACTATGAGAGAGAGAGAGAGAGATAGCAGAGAT 274
Y 1947 GGGAAAGCAGATATGGGTGAACACCCCAACTGAACTCATTTGAGAGTCCCTATGA 2006
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Db 275 GGGAAAGCAGATATGGGTGAACACCCCAACTGAACTCATTTGAGAGTCCCTATGA 334
Y 2007 GTTCAAGACTACGGTGGACAAAGTCAAGCAAGCAAACTGGCTTGGTTGGGGAC 2066
|||||
Db 335 GTTCAAGACTACGGTGGACAAAGTCAAGCAAGCAAACTGGCTTGGTTGGGGAC 394
Y 2067 CCATTTCTGAGAGGACCAAGTTTCATGAGAGCCATCAGCTCAGTCAGCAGAGGGATGAGGA 2126
Db 395 CCATTTCTGAGAGGACCAAGTTTCATGAGAGCCATCAGCTCAGTCAGCAGAGGGATGAGGA 454
Y 2127 TGAGAGTGAATCCGGGAGAGAGAGGCTCCTGCTTTGACTACATGACATTCCT 2186
|||||
Db 455 TGAGAGTGAATCCGGGAGAGAGAGGCTG-CCTCTGCTTTGACTACATGACATTCCT 513
Y 2187 GACTGTCTTCTGGAAGGCGTTTGGCTGTGTGCTCCGCCACAGATAGTCCACGCTG 2246
|||||
Db 514 GACTGTCTTCTGGAAGGCGTTTGGCTGTGTGCTCCGCCACAGATAGTCCACGCTG 573

Y 2247 GGCCTGCTCCCGCTCTCCATCCATCATT-GGCATGCTCACCGCATTCATTGGGAC 2305
|||||
Db 574 GGCCTGCTCCCGCTCTCCATCCATCATTGGGATGCTCACCGCATTCATTGGGAC 633
Y 2306 TGGCTCGCAGCTT--CGGCTCACCATTTGGTCTCAAGATTCAGTAC-AGCTGTGTTT 2362
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Db 634 TGGCTCGCAGCTTTCGGGTCTTGGCTCAAGATTCAGTACAGCTGTGTT 693
Y 2363 TCGTGGCATTTGGGACGCT 2382
Db 694 CGGGCAGTTGGGACCTT 713
RESULT 10
Bf190598 475 bp mRNA linear EST 02-NOV-2000
LOCUS Bf190598
DEFINITION 237175 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION Bf190598
VERSION Bf190598.1 GI:11073967
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.M.
and Keeler,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
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Location/Qualifiers
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Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
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Matches 433; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
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Y 2321 GCTCACCATTGCTCTCAAGATTCAGTCAAGCTGTGTTTGGTGGCATTTGGCACT 2380
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Db 61 GCTCACCATTGCTCTCAAGATTCAGTCAAGCTGTGTTTGGTGGCATTTGGCACT 120
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Db 121 CTGTGCGAGATACATTTCGCCAAGACGCCCATCCAGACGTGTATGACAGGCTT 180
 Oy 2441 CCATTGGCAACGTGACGGGAGGACGCGCTCAATGCTTCGGGATCGGCTGGCTT 2500
 Db 181 CCATTGGCAACGTGACGGGAGGACGCGCTCAACGCTTCGCGGATCGGCTGGCTT 240
 Oy 2501 GGTCCGTGGCGCCATCTACTGCGCTTCGAGGAGACAGAGTTCACAGTTCGCGCGCA 2560
 Db 241 GGTCTGTGGCGCCATCTACTGCGCTTCGAGGAGACAGAGTTCACAGTTCGCGCGCA 300
 Oy 2561 CACTGGCTTCCTCCGTCACCCCTTTCACATCTTTGATGTCGATCAGCGTCTT 2620
 Db 301 CCTGGCTTCCTCCGTCACCCCTTTCACATCTTTGATGTCGATCAGCGTCTT 360
 Oy 2621 TGTACGAGGCGGCGGACGCTGGGAGGAGGAGTTCGCGCGGCTGGGCTGCAAGCTG 2680
 Db 361 TGTACGAGGCGGCGGACGCTGGGAGGAGGAGTTCGCGCGGCTGGGCTGCAAGCTG 420
 Oy 2681 CCACACATGAGCTCTTGTGAGGCTGCGCTTCATACATCTTTGCGCACT 2735
 Db 421 CCACGACTTGGCTCTTGGAGGCTTGGCTTCATACATCTTTGCGCACT 475

RESULT 11
 BH349372/c 499 bp DNA linear GSS 03-DEC-2001
 LOCUS CH230-32M17.T3 CHORI-230 Segment 1 Rattus norvegicus genomic clone
 DEFINITION CH230-32M17, DNA sequence.
 ACCESSION BH349372
 VERSION BH349372.1 GI:17280106
 KEYWORDS GSS.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 499)
 Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,
 A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
 Jong,P. and Fraser,C.M.
 Rat BAC End Sequences from Library CHORI-230 EcORI segment
 Unpublished (1999)
 Other_GSSs: CH230-32M17.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pje@jngmail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or.oring.information.htm). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: 32 row: M column: 17
 Seq primer: SP6
 Class: BAC ends.
 FEATURES
 source
 Location/Qualifiers
 1..499
 /organism="Rattus norvegicus"
 /strain="BN/SSNHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-32M17"
 /clone_11b="CHORI-230 Segment 1"
 /sex="Female"
 /cell_type="Brain"
 /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
 CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
 Pieter de Jong"

BASE COUNT
 ORIGIN

Query Match 14.7%; Score 407.4; DB 17; Length 499;
 Best Local Similarity 91.3%; Pred. No. 3.5e-97;
 Matches 454; Conservative 0; Mismatches 41; Indels 2; Gaps 2;

Oy 361 ACCAGCAACAACACATATTCGGGCTGTGGAATGAACTGTCTCAACCTGACCTTAT-GGC 419
 Db 498 ACCAGCAACAACATATTCGGGCTGTGGAATGAACTGTCTCAACCTGACCTGATGGGC 439
 Oy 420 CTTGGGTTCTCTGCT-CTGAGATACCTCTCTTTAATTTAGAGTGTGTGTCATAGGT 478
 Db 438 CATAGGCTTTCCTGCTCCCGAGATTCCTCGCTTTAATTTAGAGTGTGTGTCATAGGT 379
 Oy 479 TCATTCGTGTGATCTGGGACCTTACCATTTAGGAGTGCAGCTTCAATGTTC 538
 Db 378 TCATTCGTGTGATTTGGGACCTTACCATTTAGGAGTGCAGCTTCAATGTTC 319
 Oy 539 TCATCATTTGATCTGTCTACGTATCCAGAGGAGACTCCAGATCAAGCATC 598
 Db 318 TCATCATTTGATCTGTCTATGTATGATCCAGATGGGAGACTCCAGATCAAGCATC 259
 Oy 599 TACGAGTCTTCTCATACCCGCTGTTGAGATCTTTGCTACATCTGGCTATATGA 658
 Db 258 TTGAGACTCTTCTGTACAGGCTGTTGAGAGCTTGTGCTATATTTGGCTCTACATGA 199
 Oy 659 TTCTGGCAGCTTCTCCCGTGTGTGTGTCAGGTTTGGAGGCTCTCTCTCTTCT 718
 Db 198 TCTTGACAGCTTCTCTCTGTTGTGTGTCAGGTTTGGAGGCTCTCTCTCTTCT 139
 Oy 719 TCTTTCAGTGTGTGTCTCTCTGCGCTGGGTGTCAGATTAACAGACTCTTCTTACAAAT 778
 Db 138 TCTTTCAGTGTGTGTCTCTCTGCGCTGGGTGTCAGATTAACAGACTCTTCTTACAAAT 79
 Oy 779 ACATGCAACAAAAGTACCGCAGACACACCGAGGAATTTATCATAGACAGAGGCTG 838
 Db 78 ACATGCAACAAAAGTACCGCAGACATTAACACCGAGGAATTTATCATAGACAGAGGCTG 19
 Oy 839 ACCACCTTAAGGCAATT 855
 Db 18 AACACCTTAAGGCAATT 2

RESULT 12
 LOCUS BC023215 3063 bp mRNA linear HTC 04-FEB-2002
 DEFINITION Homo sapiens, clone IMAGE:4932133, mRNA.
 ACCESSION BC023215
 VERSION BC023215.1 GI:18490415
 KEYWORDS HTC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 3063)
 TITLE Direct Submission
 AUTHORS Strausberg,R.
 JOURNAL Submitted (04-FEB-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT
 NIH-MGC Project URL: http://mgc.ncl.nih.gov
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huilyk, S.W., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,

Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/HLNl at: <http://image.llnl.gov>
Series: IRAC Plate: 42 Row: 9 Column: 16
This clone has the following problem: no polyA-tail.

FEATURES

source

1. 3063

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4932133"

/tissue_type="Brain, anaplastic oligodendroglioma with

1p/19q loss"

/clone_lib="NCI CGAP Brn67"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

/note="Vector: pCMV-SPORT6"

/note="Vector: pCMV-SPORT6"

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/note="Vector: pCMV-SPORT6"

/note="Vector: pCMV-SPORT6"

FEATURES

source

1. 817

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5276972"

/clone_lib="NIH_MGC_95"

/tissue_type="hippocampus"

/lab_host="DH10B"

/note="Organ: brain; Vector: Bluescript (modified

Bluescript KS+); Site:1: BamHI; Site:2: SalI; Site:3:

NotI; Oligo-dT primed using primer 5'-TTTTTTTTTTT-3',

size-selected for average insert size 2.5 kb and

normalized to ROP 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NIHRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

/note="Organ: brain; Vector: Bluescript (modified

Bluescript KS+); Site:1: BamHI; Site:2: SalI; Site:3:

NotI; Oligo-dT primed using primer 5'-TTTTTTTTTTT-3',

size-selected for average insert size 2.5 kb and

normalized to ROP 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NIHRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

/note="Organ: brain; Vector: Bluescript (modified

Bluescript KS+); Site:1: BamHI; Site:2: SalI; Site:3:

NotI; Oligo-dT primed using primer 5'-TTTTTTTTTTT-3',

size-selected for average insert size 2.5 kb and

normalized to ROP 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NIHRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

/note="Organ: brain; Vector: Bluescript (modified

Bluescript KS+); Site:1: BamHI; Site:2: SalI; Site:3:

NotI; Oligo-dT primed using primer 5'-TTTTTTTTTTT-3',

size-selected for average insert size 2.5 kb and

normalized to ROP 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NIHRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

/note="Organ: brain; Vector: Bluescript (modified

Bluescript KS+); Site:1: BamHI; Site:2: SalI; Site:3:

NotI; Oligo-dT primed using primer 5'-TTTTTTTTTTT-3',

size-selected for average insert size 2.5 kb and

normalized to ROP 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NIHRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

/note="Organ: brain; Vector: Bluescript (modified

Bluescript KS+); Site:1: BamHI; Site:2: SalI; Site:3:

NotI; Oligo-dT primed using primer 5'-TTTTTTTTTTT-3',

size-selected for average insert size 2.5 kb and

normalized to ROP 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NIHRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

/note="Organ: brain; Vector: Bluescript (modified

Bluescript KS+); Site:1: BamHI; Site:2: SalI; Site:3:

NotI; Oligo-dT primed using primer 5'-TTTTTTTTTTT-3',

size-selected for average insert size 2.5 kb and

normalized to ROP 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NIHRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

/note="Organ: brain; Vector: Bluescript (modified

Bluescript KS+); Site:1: BamHI; Site:2: SalI; Site:3:

NotI; Oligo-dT primed using primer 5'-TTTTTTTTTTT-3',

size-selected for average insert size 2.5 kb and

RESULT 14

BG819145
 LOCUS 655 bp mRNA linear EST 22-MAY-2001
 DEFINITION 602781252F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4932133
 ACCESSION BG819145
 VERSION BG819145.1 GI:14166732
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 655)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM10857 row: 9 column: 14
 High quality sequence stop: 653.
 Location/Qualifiers
 source 1..655
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4932133"
 /clone_1lb="NCI_CGAP_Brn67"
 /tissue_type="anaplastic oligodendroglioma with 1p/19q
 loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: SalI; Cloned unidirectionally. Primer: oligo dt.
 Average insert size 2.3 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 156 a 168 c 156 g 175 t
 ORIGIN
 Query Match 13.1%; Score 361.8; DB 12; Length 655;
 Best Local Similarity 97.9%; Pred. No. 5.9e-85;
 Matches 377; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
 Oy 2019 GGTGCAAACTGATGATCAAGAAAGCAAACTGGCCCTTGTGTGGGACCCATTCTG-GA 2077
 |||||||
 Db 1 GGTGCAAAACTGATGATCAAGAAAGCAAACTGGCCCTTGTGTGGGACCCATTCTGTGA 60
 Oy 2078 GGGACCACTTCATGAGAGCCATCAGCGTCAGTGCAGCAGGGGATGAGATGAGATGAAT 2137
 |||||||
 Db 61 GGGACCACTTCATGAGAGCCATCAGCGTCAGTGCAGCAGGGGATGAGATGAGATGAAT 120
 Oy 2138 CCGGGAGAGAGAGCGCCCTCCGCTTGTGACTACGTCATGCACTTCGACTGTCTCT 2197
 |||||||
 Db 121 CCGGGAGAGAGAGCGCCCTCCGCTTGTGACTACGTCATGCACTTCGACTGTCTCT 180
 Oy 2198 GGAAGGTGCTGTGTGCTGTGCCCCCAGAGAGTACTCCAGCGCTGGGCTGTTCG 2257
 |||||||
 Db 181 GGAAGGTGCTGTGTGCTGTGCCCCCAGAGAGTACTCCAGCGCTGGGCTGTTCG 240
 Oy 2258 CGCTTCATTCATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 2317
 |||||||
 Db 241 CGCTTCATTCATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 300
 Oy 2318 TCGGCTGCACCATTCGCTCAAGAAATTCATCAGCTGTGTTTTCGTGGCAATTTGGCA 2377
 |||||||
 Db 301 TCGGCTGCACCATTCGCTCAAGAAATTCATCAGCTGTGTTTTCGTGGCAATTTGGCA 360
 Oy 2378 CTTCTGTCCAGATACGTTTGGCAG 2402
 |||||||
 Db 361 CTTCTGTCCAGATACGTTTGGCAG 385

RESULT 15
 BG293782
 LOCUS 677 bp mRNA linear EST 21-FEB-2001
 DEFINITION 602390677F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4502515 5',
 mRNA sequence.
 ACCESSION BG293782
 VERSION BG293782.1 GI:13053790
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 677)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM10371 row: 1 column: 20
 High quality sequence start: 14
 High quality sequence stop: 676.
 Location/Qualifiers
 source 1..677
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:4502515"
 /clone_1lb="NIH_MGC_94"
 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: SalI; Cloned unidirectionally; oligo-dt primed.
 Average insert size 3.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."
 BASE COUNT 176 a 153 c 198 g 150 t
 ORIGIN
 Query Match 13.0%; Score 359.4; DB 12; Length 677;
 Best Local Similarity 93.3%; Pred. No. 2.6e-84;
 Matches 419; Conservative 0; Mismatches 26; Indels 4; Gaps 4;
 Oy 1785 GAAACCATTAAGGTTTAAATAGTAGTGAAGAGAAATACGAAGCAAGATTTCTT 1844
 |||||||
 Db 227 GAAACCATTAAGGTTTAAATAGTAGTGAAGAGAAATACGAAGCAAGATTTCTT 286
 Oy 1845 CATTGCCCTTGTGTAACCGAATGATGTAAGCGTAATTCAGATGTGCACAGAGAA 1904
 |||||||
 Db 287 CATTGCCCTTGTGTAACCGAATGATGTAAGCGTAATTCAGATGTGCACAGAGAA 346
 Oy 1905 GCTGACTATGGA-AGAAGAGAGAGCCCAAGAGATAGCAGAG-ATGGGAAAGCCAGTATTTG 1962
 |||||||
 Db 347 GCTGACTATGGA-AGAAGAGAGAGCCCAAGAGATAGCAGAGATAGGAAAGCCAGTATTTG 406
 Oy 1963 GGTGAACACCCCAACTAGATCATTTGAA-GAATCCTATGAGTTCAAGACTACGGT 2021
 |||||||
 Db 407 GGTGAACACCCCAACTAGATCATTTGAA-GAATCCTATGAGTTCAAGAGTAACTAGT 466
 Oy 2022 GGCAAACTGATCAAGAAAGCAAACTGGCCCTTGTGTGGGACCCATTCTGAGAGGA 2081
 |||||||
 Db 467 GGATTAAGCTATCAAGAAAGCAAACTGGCCATTGTTGTGGGACCCATTCTGAGAGGA 526
 Oy 2082 CCAATTGATGAGAGCCATTCACCGTCAGCAGAGAGGATGAGATGAGATGAGATTCGG 2141
 |||||||
 Db 527 CCAATTGATGAGAGCCATTCACCGTCAGCAGAGAGGATGAGATGAGATGAGATTCGG 586

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OY 2142 GGAGGAGAGGCTGCCCTCTCTGCTTTGACTACATGCACTTCTGACTGTCTTGAA 2201
    |||||||
Db 587 AGAGGAGAGGCTGCCATCTCTTTGACTACATGCACTTCTGAGGTCCTTGAA 646
    |||||||
OY 2202 GGTCGTGTTGCTGTGTCGCCCCCAG 2230
    |||||||
Db 647 GGTCCT-CTTGCCTGTGTGCCCCCAAG 674
    |||||||

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Search completed: November 30, 2002, 12:23:11
 Job time : 2560 secs